

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=12; day=11; hr=14; min=44; sec=54; ms=967;
]

=====

Application No: 10593841 Version No: 2.0

Input Set:

Output Set:

Started: 2008-11-26 10:13:56.207
Finished: 2008-11-26 10:13:57.942
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 735 ms
Total Warnings: 4
Total Errors: 0
No. of SeqIDs Defined: 27
Actual SeqID Count: 27

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)

SEQUENCE LISTING

<110> Heidner, Hans Walter
 Klimstra, William Brown
 Ryman, Katherine Diana

<120> METHODS AND COMPOSITIONS COMPRISING PROTEIN L IMMUNOGLOBULIN
 BINDING DOMAINS FOR CELL-SPECIFIC TARGETING

<130> 9568-2

<140> 10593841
 <141> 2008-11-26

<150> PCT/US2004/013281
 <151> 2004-04-29

<160> 27

<170> PatentIn version 3.3

<210> 1
 <211> 2657
 <212> DNA
 <213> Peptostreptococcus magnus

<220>
 <221> CDS
 <222> (301)..(2460)
 <223> protein L

<220>
 <221> repeat_unit
 <222> (592)..(819)
 <223> PpL1

<220>
 <221> repeat_unit
 <222> (820)..(1035)
 <223> PpL2

<220>
 <221> repeat_unit
 <222> (1036)..(1251)
 <223> PpL3

<220>
 <221> repeat_unit
 <222> (1252)..(1467)
 <223> PpL4

<220>
 <221> repeat_unit
 <222> (1468)..(1686)
 <223> PpL5

```

<400> 1
atagtgtctac aataaaggat ggactgaac taccgaacct aacgcttggtg gacattgtct      60

tgggaaattht ggacagtggg cgaatcaaga acaccattaa ttaaattggt gaagttcgat      120

tgttgatcac ccttttttggg taaacaataa ctaaggaatg gcaatatatt tgcttggaaa      180

cgaatttgat ttaaatagca ttgaatgcaa aaaaatttaa aaggaggaga caaattccac      240

ccttattaga agggaagttt ccattgtcat gatattatga aaattaataa gaaattatta      300

atg gct gca ctt gca ggt gca att gta gta aca ggt gga gta gga tct      348
Met Ala Ala Leu Ala Gly Ala Ile Val Val Thr Gly Gly Val Gly Ser
1          5          10          15

tac gca gct gat gaa cct att gat ctt gaa aaa ctt gaa gaa aaa agg      396
Tyr Ala Ala Asp Glu Pro Ile Asp Leu Glu Lys Leu Glu Glu Lys Arg
          20          25          30

gat aaa gaa aat gta gga aat tta cca aaa ttc gat aat gaa gtt aaa      444
Asp Lys Glu Asn Val Gly Asn Leu Pro Lys Phe Asp Asn Glu Val Lys
          35          40          45

gat ggt tca gaa aat cca atg gct aaa tat cca gat ttc gat gat gaa      492
Asp Gly Ser Glu Asn Pro Met Ala Lys Tyr Pro Asp Phe Asp Asp Glu
          50          55          60

gcc agt aca aga ttt gaa aca gaa aac aat gaa ttt gaa gaa aaa aaa      540
Ala Ser Thr Arg Phe Glu Thr Glu Asn Asn Glu Phe Glu Glu Lys Lys
65          70          75          80

gtt gtt tct gat aac ttt ttt gat caa tca gaa cat ccg ttt gta gaa      588
Val Val Ser Asp Asn Phe Phe Asp Gln Ser Glu His Pro Phe Val Glu
          85          90          95

aat aaa gaa gaa aca cca gaa aca cca gaa act gat tca gaa gaa gaa      636
Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu
          100          105          110

gta aca atc aaa gct aac cta atc ttt gca aat gga agc aca caa act      684
Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr
          115          120          125

gca gaa ttc aaa gga aca ttt gaa aaa gca aca tca gaa gct tat gcg      732
Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala
          130          135          140

tat gca gat act ttg aag aaa gac aat gga gaa tat act gta gat gtt      780
Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val
145          150          155          160

gca gat aaa ggt tat act tta aat att aaa ttt gct gga aaa gaa aaa      828
Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys
          165          170          175

aca cca gaa gaa cca aaa gaa gaa gtt act att aaa gca aac tta atc      876

```

Thr	Pro	Glu	Glu	Pro	Lys	Glu	Glu	Val	Thr	Ile	Lys	Ala	Asn	Leu	Ile	
			180					185					190			
tat	gca	gat	gga	aaa	aca	caa	aca	gca	gaa	ttc	aaa	gga	aca	ttt	gaa	924
Tyr	Ala	Asp	Gly	Lys	Thr	Gln	Thr	Ala	Glu	Phe	Lys	Gly	Thr	Phe	Glu	
		195					200					205				
gaa	gca	aca	gca	gaa	gca	tac	aga	tat	gca	gat	gca	tta	aag	aag	gac	972
Glu	Ala	Thr	Ala	Glu	Ala	Tyr	Arg	Tyr	Ala	Asp	Ala	Leu	Lys	Lys	Asp	
	210					215				220						
aat	gga	gaa	tat	aca	gta	gac	gtt	gca	gat	aaa	ggt	tat	act	tta	aat	1020
Asn	Gly	Glu	Tyr	Thr	Val	Asp	Val	Ala	Asp	Lys	Gly	Tyr	Thr	Leu	Asn	
225					230				235						240	
att	aaa	ttt	gct	gga	aaa	gaa	aaa	aca	cca	gaa	gaa	cca	aaa	gaa	gaa	1068
Ile	Lys	Phe	Ala	Gly	Lys	Glu	Lys	Thr	Pro	Glu	Glu	Pro	Lys	Glu	Glu	
			245					250					255			
gtt	act	att	aaa	gca	aac	tta	atc	tat	gca	gat	gga	aaa	aca	caa	aca	1116
Val	Thr	Ile	Lys	Ala	Asn	Leu	Ile	Tyr	Ala	Asp	Gly	Lys	Thr	Gln	Thr	
			260				265						270			
gca	gaa	ttc	aaa	gga	aca	ttt	gaa	gaa	gca	aca	gca	gaa	gca	tac	aga	1164
Ala	Glu	Phe	Lys	Gly	Thr	Phe	Glu	Glu	Ala	Thr	Ala	Glu	Ala	Tyr	Arg	
	275					280					285					
tat	gct	gac	tta	tta	gca	aaa	gaa	aat	ggt	aaa	tat	aca	gta	gac	gtt	1212
Tyr	Ala	Asp	Leu	Leu	Ala	Lys	Glu	Asn	Gly	Lys	Tyr	Thr	Val	Asp	Val	
	290					295				300						
gca	gat	aaa	ggt	tat	act	tta	aat	att	aaa	ttt	gct	gga	aaa	gaa	aaa	1260
Ala	Asp	Lys	Gly	Tyr	Thr	Leu	Asn	Ile	Lys	Phe	Ala	Gly	Lys	Glu	Lys	
305					310				315					320		
aca	cca	gaa	gaa	cca	aaa	gaa	gaa	gtt	act	att	aaa	gca	aac	tta	atc	1308
Thr	Pro	Glu	Glu	Pro	Lys	Glu	Glu	Val	Thr	Ile	Lys	Ala	Asn	Leu	Ile	
			325					330					335			
tat	gca	gat	gga	aaa	act	caa	aca	gca	gag	ttc	aaa	gga	aca	ttt	gca	1356
Tyr	Ala	Asp	Gly	Lys	Thr	Gln	Thr	Ala	Glu	Phe	Lys	Gly	Thr	Phe	Ala	
		340					345					350				
gaa	gca	aca	gca	gaa	gca	tac	aga	tac	gct	gac	tta	tta	gca	aaa	gaa	1404
Glu	Ala	Thr	Ala	Glu	Ala	Tyr	Arg	Tyr	Ala	Asp	Leu	Leu	Ala	Lys	Glu	
	355					360					365					
aat	ggt	aaa	tat	aca	gca	gac	tta	gaa	gat	ggt	gga	tac	act	att	aat	1452
Asn	Gly	Lys	Tyr	Thr	Ala	Asp	Leu	Glu	Asp	Gly	Gly	Tyr	Thr	Ile	Asn	
	370					375					380					
att	aga	ttt	gca	ggt	aag	aaa	gtt	gac	gaa	aaa	cca	gaa	gaa	aaa	gaa	1500
Ile	Arg	Phe	Ala	Gly	Lys	Lys	Val	Asp	Glu	Lys	Pro	Glu	Glu	Lys	Glu	
385					390				395						400	
caa	gta	aca	att	aaa	gaa	aat	ata	tat	ttt	gaa	gat	gga	aca	gta	caa	1548
Gln	Val	Thr	Ile	Lys	Glu	Asn	Ile	Tyr	Phe	Glu	Asp	Gly	Thr	Val	Gln	

405	410	415	
act gca aca ttt aaa gga aca ttt gca gaa gcg aca gca gaa gca tac			1596
Thr Ala Thr Phe Lys Gly Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr			
420	425	430	
aga tat gca gat ttg tta tca aaa gaa cat ggt aaa tac aca gca gac			1644
Arg Tyr Ala Asp Leu Leu Ser Lys Glu His Gly Lys Tyr Thr Ala Asp			
435	440	445	
ttg gaa gat ggt gga tac act atc aac att aga ttt gct gga aaa gaa			1692
Leu Glu Asp Gly Gly Tyr Thr Ile Asn Ile Arg Phe Ala Gly Lys Glu			
450	455	460	
gaa cca gaa gaa aca cca gaa aaa cca gaa gta caa gac gga tat gca			1740
Glu Pro Glu Glu Thr Pro Glu Lys Pro Glu Val Gln Asp Gly Tyr Ala			
465	470	475	480
tca tac gaa gaa gct gaa gca gca gct aaa gaa gct ttg aaa aat gat			1788
Ser Tyr Glu Glu Ala Glu Ala Ala Ala Lys Glu Ala Leu Lys Asn Asp			
485	490	495	
gat gta aat aaa tca tat act att aga caa ggt gca gat gga aga tat			1836
Asp Val Asn Lys Ser Tyr Thr Ile Arg Gln Gly Ala Asp Gly Arg Tyr			
500	505	510	
tac tat gta tta tca cca gta gaa gct gaa gaa gaa aaa cca gaa gca			1884
Tyr Tyr Val Leu Ser Pro Val Glu Ala Glu Glu Glu Lys Pro Glu Ala			
515	520	525	
caa aat gga tat gca aca tac gaa gaa gca gaa gca gca gct aag aaa			1932
Gln Asn Gly Tyr Ala Thr Tyr Glu Glu Ala Glu Ala Ala Ala Lys Lys			
530	535	540	
gct ttg gaa aat gat cca atc aat aaa tct tac agc ata aga caa ggt			1980
Ala Leu Glu Asn Asp Pro Ile Asn Lys Ser Tyr Ser Ile Arg Gln Gly			
545	550	555	560
gca gat gga aga tac tac tat gta tta tca cca gta gaa gct gaa act			2028
Ala Asp Gly Arg Tyr Tyr Tyr Val Leu Ser Pro Val Glu Ala Glu Thr			
565	570	575	
cct gaa aaa cca gta gaa cca tca gaa cca tca aca cca gat gta cca			2076
Pro Glu Lys Pro Val Glu Pro Ser Glu Pro Ser Thr Pro Asp Val Pro			
580	585	590	
tca aac cca tca aat cca tca aca cca gat gtt cca tca act cct gat			2124
Ser Asn Pro Ser Asn Pro Ser Thr Pro Asp Val Pro Ser Thr Pro Asp			
595	600	605	
gta cca tca aat cct tca act cca gaa gtt cct tca aac cca tca act			2172
Val Pro Ser Asn Pro Ser Thr Pro Glu Val Pro Ser Asn Pro Ser Thr			
610	615	620	
cct ggt aat gaa gaa aaa cct ggt aac gaa caa aaa cct ggt aac gaa			2220
Pro Gly Asn Glu Glu Lys Pro Gly Asn Glu Gln Lys Pro Gly Asn Glu			
625	630	635	640

caa aaa cct ggt aac gaa caa aaa cct ggt aat gaa caa aaa cct ggt 2268
Gln Lys Pro Gly Asn Glu Gln Lys Pro Gly Asn Glu Gln Lys Pro Gly
645 650 655

aat gaa caa aaa cca gac caa cct tca aaa cca gaa aaa gaa gaa aat 2316
Asn Glu Gln Lys Pro Asp Gln Pro Ser Lys Pro Glu Lys Glu Glu Asn
660 665 670

ggt aag ggt gga gta gat tct cca aag aaa aaa gaa aaa gct gca tta 2364
Gly Lys Gly Gly Val Asp Ser Pro Lys Lys Lys Glu Lys Ala Ala Leu
675 680 685

cca aaa gct ggt agc gaa gct gaa atc tta aca tta gca gca gct tca 2412
Pro Lys Ala Gly Ser Glu Ala Glu Ile Leu Thr Leu Ala Ala Ala Ser
690 695 700

tta tca agc gtt gca ggt gct ttc att tca ctt aaa aaa cgt aaa taa 2460
Leu Ser Ser Val Ala Gly Ala Phe Ile Ser Leu Lys Lys Arg Lys
705 710 715

ttaatcttag ataaaaaata gattaatcta aaaaaatggg acttttataa gtcccatttt 2520

tgattgcaat gaaactgata caaaaaatgt atcagttttt tcatttacgc ttattttcct 2580

gtgagtatgt ccaagtttgt cgtataatca tctatcaaaa gcctggcgag tttecgctttt 2640

tggattttgt cttcgaa 2657

<210> 2
<211> 719
<212> PRT
<213> Peptostreptococcus magnus

<400> 2

Met Ala Ala Leu Ala Gly Ala Ile Val Val Thr Gly Gly Val Gly Ser
1 5 10 15

Tyr Ala Ala Asp Glu Pro Ile Asp Leu Glu Lys Leu Glu Glu Lys Arg
20 25 30

Asp Lys Glu Asn Val Gly Asn Leu Pro Lys Phe Asp Asn Glu Val Lys
35 40 45

Asp Gly Ser Glu Asn Pro Met Ala Lys Tyr Pro Asp Phe Asp Asp Glu
50 55 60

Ala Ser Thr Arg Phe Glu Thr Glu Asn Asn Glu Phe Glu Glu Lys Lys
65 70 75 80

Val	Val	Ser	Asp	Asn	Phe	Phe	Asp	Gln	Ser	Glu	His	Pro	Phe	Val	Glu	
				85					90					95		
Asn	Lys	Glu	Glu	Thr	Pro	Glu	Thr	Pro	Glu	Thr	Asp	Ser	Glu	Glu	Glu	
			100					105					110			
Val	Thr	Ile	Lys	Ala	Asn	Leu	Ile	Phe	Ala	Asn	Gly	Ser	Thr	Gln	Thr	
		115					120					125				
Ala	Glu	Phe	Lys	Gly	Thr	Phe	Glu	Lys	Ala	Thr	Ser	Glu	Ala	Tyr	Ala	
	130					135					140					
Tyr	Ala	Asp	Thr	Leu	Lys	Lys	Asp	Asn	Gly	Glu	Tyr	Thr	Val	Asp	Val	
145					150					155					160	
Ala	Asp	Lys	Gly	Tyr	Thr	Leu	Asn	Ile	Lys	Phe	Ala	Gly	Lys	Glu	Lys	
			165						170					175		
Thr	Pro	Glu	Glu	Pro	Lys	Glu	Glu	Val	Thr	Ile	Lys	Ala	Asn	Leu	Ile	
			180					185					190			
Tyr	Ala	Asp	Gly	Lys	Thr	Gln	Thr	Ala	Glu	Phe	Lys	Gly	Thr	Phe	Glu	
		195					200					205				
Glu	Ala	Thr	Ala	Glu	Ala	Tyr	Arg	Tyr	Ala	Asp	Ala	Leu	Lys	Lys	Asp	
	210					215					220					
Asn	Gly	Glu	Tyr	Thr	Val	Asp	Val	Ala	Asp	Lys	Gly	Tyr	Thr	Leu	Asn	
225					230					235					240	
Ile	Lys	Phe	Ala	Gly	Lys	Glu	Lys	Thr	Pro	Glu	Glu	Pro	Lys	Glu	Glu	
			245						250					255		
Val	Thr	Ile	Lys	Ala	Asn	Leu	Ile	Tyr	Ala	Asp	Gly	Lys	Thr	Gln	Thr	
			260					265					270			
Ala	Glu	Phe	Lys	Gly	Thr	Phe	Glu	Glu	Ala	Thr	Ala	Glu	Ala	Tyr	Arg	
		275					280					285				
Tyr	Ala	Asp	Leu	Leu	Ala	Lys	Glu	Asn	Gly	Lys	Tyr	Thr	Val	Asp	Val	
	290					295					300					
Ala	Asp	Lys	Gly	Tyr	Thr	Leu	Asn	Ile	Lys	Phe	Ala	Gly	Lys	Glu	Lys	

305		310		315		320									
Thr	Pro	Glu	Glu	Pro	Lys	Glu	Glu	Val	Thr	Ile	Lys	Ala	Asn	Leu	Ile
				325					330					335	
Tyr	Ala	Asp	Gly	Lys	Thr	Gln	Thr	Ala	Glu	Phe	Lys	Gly	Thr	Phe	Ala
			340					345					350		
Glu	Ala	Thr	Ala	Glu	Ala	Tyr	Arg	Tyr	Ala	Asp	Leu	Leu	Ala	Lys	Glu
		355					360					365			
Asn	Gly	Lys	Tyr	Thr	Ala	Asp	Leu	Glu	Asp	Gly	Gly	Tyr	Thr	Ile	Asn
	370					375					380				
Ile	Arg	Phe	Ala	Gly	Lys	Lys	Val	Asp	Glu	Lys	Pro	Glu	Glu	Lys	Glu
385					390					395					400
Gln	Val	Thr	Ile	Lys	Glu	Asn	Ile	Tyr	Phe	Glu	Asp	Gly	Thr	Val	Gln
				405					410					415	
Thr	Ala	Thr	Phe	Lys	Gly	Thr	Phe	Ala	Glu	Ala	Thr	Ala	Glu	Ala	Tyr
			420					425					430		
Arg	Tyr	Ala	Asp	Leu	Leu	Ser	Lys	Glu	His	Gly	Lys	Tyr	Thr	Ala	Asp
		435					440					445			
Leu	Glu	Asp	Gly	Gly	Tyr	Thr	Ile	Asn	Ile	Arg	Phe	Ala	Gly	Lys	Glu
	450					455					460				
Glu	Pro	Glu	Glu	Thr	Pro	Glu	Lys	Pro	Glu	Val	Gln	Asp	Gly	Tyr	Ala
465					470					475					480
Ser	Tyr	Glu	Glu	Ala	Glu	Ala	Ala	Ala	Lys	Glu	Ala	Leu	Lys	Asn	Asp
				485					490					495	
Asp	Val	Asn	Lys	Ser	Tyr	Thr	Ile	Arg	Gln	Gly	Ala	Asp	Gly	Arg	Tyr
			500					505					510		
Tyr	Tyr	Val	Leu	Ser	Pro	Val	Glu	Ala	Glu	Glu	Glu	Lys	Pro	Glu	Ala
		515					520					525			
Gln	Asn	Gly	Tyr	Ala	Thr	Tyr	Glu	Glu	Ala	Glu	Ala	Ala	Ala	Lys	Lys
	530					535					540				

Ala Leu Glu Asn Asp Pro Ile Asn Lys Ser Tyr Ser Ile Arg Gln Gly
545 550 555 560

Ala Asp Gly Arg Tyr Tyr Tyr Val Leu Ser Pro Val Glu Ala Glu Thr
565 570 575

Pro Glu Lys Pro Val Glu Pro Ser Glu Pro Ser Thr Pro Asp Val Pro
580 585 590

Ser Asn Pro Ser Asn Pro Ser Thr Pro Asp Val Pro Ser Thr Pro Asp
595 600 605

Val Pro Ser Asn Pro Ser Thr Pro Glu Val Pro Ser Asn Pro Ser Thr
610 615 620

Pro Gly Asn Glu Glu Lys Pro Gly Asn Glu Gln Lys Pro Gly Asn Glu
625 630 635 640

Gln Lys Pro Gly Asn Glu Gln Lys Pro Gly Asn Glu Gln Lys Pro Gly
645 650 655

Asn Glu Gln Lys Pro Asp Gln Pro Ser Lys Pro Glu Lys Glu Glu Asn
660 665 670

Gly Lys Gly Gly Val Asp Ser Pro Lys Lys Lys Glu Lys Ala Ala Leu
675 680 685

Pro Lys Ala Gly Ser Glu Ala Glu Ile Leu Thr Leu Ala Ala Ala Ser
690 695 700

Leu Ser Ser Val Ala Gly Ala Phe Ile Ser Leu Lys Lys Arg Lys
705 710 715